

SEQUENCE LISTING

<110> Miller, Duane D.

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<120> LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF  
USE

<130> 20609/181

<140>

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<150> 60/190,370

<151> 2000-03-17

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 1095

<212> DNA

<213> Homo sapiens

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Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe  
65 70 75 80  
  
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Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Ala Ile Ala Ile  
130 135 140  
  
Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser  
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Asn Arg Arg Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile  
165 170 175

Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile  
180 185 190

Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val  
195 200 205

Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu  
210 215 220

Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser  
225 230 235 240

Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu  
245 250 255

Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr  
260 265 270

Pro Gly Leu Val Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp  
275 280 285

Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser  
290 295 300

Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala  
305 310 315 320

Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly  
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25

30

Val	Val	Val	Val	Ala	Leu	Gly	Leu	Thr	Val	Ser	Val	Leu	Val	Leu	Leu

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Thr	Asn	Leu	Leu	Val	Ile	Ala	Ala	Ile	Ala	Ser	Asn	Arg	Arg	Phe	His

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55

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Gln	Pro	Ile	Tyr	Tyr	Leu	Leu	Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Phe

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Ala	Gly	Val	Ala	Tyr	Leu	Phe	Leu	Met	Phe	His	Thr	Gly	Pro	Arg	Thr

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Ala	Arg	Leu	Ser	Leu	Glu	Gly	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp

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105

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Thr	Ser	Leu	Thr	Ala	Ser	Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala	Val	Glu

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Arg	His	Arg	Ser	Val	Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu	Pro	Arg

130

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140

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145 150 155 160

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165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val  
180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr  
195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu  
210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val  
225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro  
245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn  
260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser  
275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg  
290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg  
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130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr  
180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg  
195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr  
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln  
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val  
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met  
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro  
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln  
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gtgaatagta cagctgtgcc cacaacacca gcagcattt agagcctaa cttgccttt 240  
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25

30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe

35

40

45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr

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55

60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu

65

70

75

80

Gln	Ile	Thr	Leu	Ser	Ala	Ile	Met	Ile	Phe	Ile	Leu	Phe	Val	Ser	Phe
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Arg	Ser	Ala	Ile	Asn	Ile	Leu	Leu	Ala	Ser	Leu	Ala	Phe	Ala	Asp	Met
							115		120			125			
Leu	Leu	Ala	Val	Leu	Asn	Met	Pro	Phe	Ala	Leu	Val	Thr	Ile	Leu	Thr
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Thr	Arg	Trp	Ile	Phe	Gly	Lys	Phe	Phe	Cys	Arg	Val	Ser	Ala	Met	Phe
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Phe	Trp	Leu	Phe	Val	Ile	Glu	Gly	Val	Ala	Ile	Leu	Leu	Ile	Ile	Ser
						165			170			175			
Ile	Asp	Arg	Phe	Leu	Ile	Ile	Val	Gln	Arg	Gln	Asp	Lys	Leu	Asn	Pro
						180			185			190			
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Ala	Tyr	Val	Ile	Leu	Ile	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Pro	Phe	Leu
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Val	Ile	Leu	Tyr	Ser	Phe	Met	Gly	Ile	Leu	Asn	Thr	Leu	Arg	His	Asn
						260			265			270			
Ala	Leu	Arg	Ile	His	Ser	Tyr	Pro	Glu	Gly	Ile	Cys	Leu	Ser	Gln	Ala
						275			280			285			
Ser	Lys	Leu	Gly	Leu	Met	Ser	Leu	Gln	Arg	Pro	Phe	Gln	Met	Ser	Ile
						290			295			300			
Asp	Met	Gly	Phe	Lys	Thr	Arg	Ala	Phe	Thr	Thr	Ile	Leu	Ile	Leu	Phe
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Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile  
340 345 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro  
355 360 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp  
370 375 380

Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr  
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<212> DNA

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<210> 10

<211> 20

<212> DNA

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<210> 12

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<210> 16  
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<210> 17  
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<210> 18  
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<210> 19  
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<210> 23  
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<220>  
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<210> 24  
<211> 23  
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<210> 26  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer,  
reverse PSP24

<400> 26  
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